Amendments to the claims:

Please amend claims 1, 3-13, 15, 28, 29 and 33, as follows:

1. (Currently Amended) A composition comprising a substantially purified thermostable AviIII peptide, said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70% identity to SEQ ID NO. 3 and a carbohydrate binding domain (CBD) III, the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO 3 in each conserved position marked by an asterisk (*), as shown below in comparison to Aspergillus aculeatus Avicelase III (AviIII_Ace):

GH74 Ace	ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac	AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
	::.***.**. **** *. ***** .* *: *.***** ** :: : * **:****
GH74_Ace	WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG
	:.* *: ::*:**::*:.********* *:**** *: ****
GH74_Ace	GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYFQDSSS

GH74 Ace	TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII Aac	TYTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
	* * ** *: .**: * * .* * .* * . * . * . *
GH74 Ace	GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF
AviIII Aac	GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISPTSLASTYY
	:**:.* ::.**::* .****:.* * *:.:***.** *** *
GH74 Ace	GYSGLTIDROHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac	GYGGLSVDLOVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
	.::* * *.*:***: .**** :*****: **:*** * ***
GH74 Ace	AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII Aac	NAPWIQDTTSTDQFPVRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
	:: ::* **:****:*: **** *:*. :***:***
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AviIII_Aac	TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI
	: .:. *:** ** .**:**.**:** *** *:*: * : :*.: *:
GH74 Ace	DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac	DYAGNKPSNIVRSGASDDYPTLALSSNFGSTWYADYAASTSTGTGAVALSADGDT
	*** :** ***:*: * . :*:*:: **: * *:** ****.
GH74 Ace	FVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII Aac	VLLMSSTSGALVSKSQGTLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT
	.: * * : * : : :: * : : * * . :
GH74_Ace	TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII Aac	SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
	:*; * ** :*; * *. **:* ::**:**: **::: * :**::

GH74 Ace	GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII Aac	GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
	****::** .:: . **.*.:* ::*.*.* :*.* .* :*:** .
GH74_Ace	LRRVYIGTNGRGIVYGDIGGAPSG
AviIII Aac	YGRVFRGHERPGHLLRQSQREPAG
	**: * : * : *:* .

- 2. (Currently Amended) The composition of claim 1 wherein the thermostable AviIII peptide is further defined as comprising a linker and a signal sequence.
- 3. (Cancelled) The composition of claim 1 or 2 wherein the glycosyl hydrolase family 74 enzyme catalytic domain of the thermostable AviIII peptide is further defined as having a length of about 730 to about 760 amino acids.
- 4. (Currently Amended) The composition of claim 1, 2, or 3 1 or 2 wherein the carbohydrate binding domain (CBD) III of the thermostable AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
- 5. (Currently Amended) The composition of claim 1,2, or 3 1 or 2 wherein the carbohydrate binding domain (CBD) III of the thermostable AviIII peptide is further defined as comprising a length of about 90 amino acids.
- 6. (Currently Amended) The composition of claim 3 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as <u>including</u> a polypeptide sequence of <u>identical to SEQ ID NO: 3</u>.
- 7. (Currently Amended) The composition of claim 3 1 wherein the carbohydrate binding domain (CBD) III is further defined as a polypeptide sequence of SEQ ID NO: 4.
- 8. (Previously Amended) The composition of claim 3 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

- 9. (Currently Amended) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides represented by of-SEQ ID NO: 3 and SEQ ID NO: 4.
- 10. (Currently Amended) The composition of claim 1, wherein said AviIII protein is encoded by a nucleic acid sequence having the catalytic domain GH74_Ace including at least about 8090% sequence identity to the polynucleotide sequence of SEQ ID NO: 23..
- 11. (Currently Amended) The composition of claim 1 wherein said AviIII

 protein is encoded by a nucleic acid sequence having the catalytic domain GH74

 including at least about 80% sequence identity to the polynucleotide sequence of SEQ ID

 NO: 23.
- 12. (Previously Amended) An isolated thermostable AviIII peptide having a polypeptide sequence of SEQ ID NO: 1.
 - 13. (Cancelled)
- 14. (Currently Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the thermostable AviIII polypeptide of claim 1.
- 15. The industrial mixture of claim 14 further defined as comprising a detergent.

 [1] Amus 16-27 (Cancelled)
- 28. (Currently Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected fort he group consisting of:
 - a) a polypeptide sequence of SEQ ID NO: 3;
 - b) a polypeptide sequence of SEQ ID NO: 4;
 - c) a polypeptide sequence of SEQ ID NO: 5;

- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof a polypeptide sequence of SEQ ID NO: 3; SEQ ID NO: 4; and SEQ ID NO: 5; or

f) a sequence having at least about 70% sequence identity with the polypeptide sequence of a), b), c), d), or e).

- 29. (Cancelled)
- 30. A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.
- 31. The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.
- 32. The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.
- 33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, glutathione S-transferase, or OmpA signal sequence tag.
- 34. The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.
 - 35. The fusion protein of claim 34, wherein the agent is a leucine zipper.
- 36. A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose. 37-42(Cancelled)
- 43. A composition comprising the polypeptide molecule of claim 28 and a carrier.